

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 21:05:24 ; Search time 1445 Seconds

Perfect score: 90 (without alignments)
Sequence: 1 gggagacggccgggtggcg.....cggtgtccccgcggcagggtcg 90

Scoring table: IDENTITY_NUC
Gapon 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lassing first 45 summaries
Database : EST:*

1: em_estba:*

2: em_estthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfan:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_livv:*

20: em_gss_pin:*

21: em_gss_yrt:*

22: em_gss_fan:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_ror:*

RESULT 1
AU098678

LOCUS AU098678 Sugano Homo sapiens cDNA library Homo sapiens mRNA clone
DEFINITION COL6158 similar to Human mRNA for amyloid A4 precursor of Alzheimer's disease, mRNA sequence.
ACCESSION AU098678
VERSION AU098678.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 300)
AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hara
, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
, K., Suyama,A. and Sugano,S.
TITLE In silico mapping of the 5'-ends of human mRNAs using full-length
enriched and 5'-end enriched cDNA libraries constructed by
Oligo-capping method
Unpublished (2001)

JOURNAL

COMMENT Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
, S., Construction and characterization of a full length enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	90	100.0	300	9 AU098678	AU098678
2	90	100.0	350	12 BE831859	BE831859
3	90	100.0	447	14 BM694414	BM694414
4	90	100.0	571	13 BI547746	BI547746
5	90	100.0	635	13 BI547550	BI547550
6	90	100.0	653	9 AL042549	AL042549 DRFP434I

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	90	100.0	300	9 AU098678	AU098678
2	90	100.0	350	12 BE831859	BE831859
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4	90	100.0	571	13 BI547746	BI547746
5	90	100.0	635	13 BI547550	BI547550
6	90	100.0	653	9 AL042549	AL042549 DRFP434I

FEATURES	source	Location/Qualifiers	BASE COUNT	60 a	114 c	104 g	71 t	1 others
		1. .300 /organism="Homo sapiens" /db_xref="Jaxom:1606", /clone="COF09158", /clone.lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"	Query Match	100.0%	Score 90; DB 12;	Length 350;		
BASE COUNT	50 a	86 c 112 g 52 t	Best Local Similarity	100.0%	Score 90; DB 9;	Length 300;	0; Mismatches 0;	Indels 0; Gaps 0;
ORIGIN			Matches	90;	Pred. No. 6.2e-13;			
Qy	1	GGAGACCTCGGCCCCGGCGAGGAGCAGGGATCCACTGGCACA 60	Qy	1	GGGAGACCTCGGCCCCGGCGAGGAGCAGGGATCCACTGGCACA 60	Qy	1	GGGAGACCTCGGCCCCGGCGAGGAGCAGGGATCCACTGGCACA 274
Db	56	GGAGACCTCGGCCCCGGCGAGGAGCAGGGATCCACTGGCACA 90	Db	333	GGGAGACCTCGGCCCCGGCGAGGAGCAGGGATCCACTGGCACA 274	Db	273	GCACGCACACTCGGCCCCGGCGAGGAGCAGGGATCCACTGGCACA 244
RESULT 3			LOCUS	BM694414	447 bp	mRNA	linear EST 28-FEB-2002	
			DEFINITION	UI-E-CII-afq-d-05-0-UI.r1	UI-E-CII Homo sapiens cDNA clone			
			ACCESSION	BM694414	UI-E-CII-afq-d-05-0-UI 5,	mRNA sequence.		
			KEYWORDS	BM694414.1	GI:19007672			
			SOURCE	EST.				
			ORGANISM	Homo sapiens				
				Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RESULT 2			COMMENT	1 (bases 1 to 447)				
BB831859			REFERENCE	BM694414	Normalization and subtraction: two approaches to facilitate gene			
LOCUS	BE831859	350 bp	AUTHORS	Bonaldo,M.P., Lennon,G. and Soares,M.B.				
DEFINITION	RC6-MT0061-310700-021-G04 MT0061	mRNA	TITLE					
ACCESSION	BE831859	linear	JOURNAL	Genome Res.	6 (9), 791-806 (1996)			
VERSION	BE831859.1	Homo sapiens cDNA, mRNA sequence.	COMMENT	9704477				
KEYWORDS	GI:10264237		CONTACT	Soares, MB				
SOURCE	EST.		Program for Rat Gene Discovery and Mapping					
ORGANISM	Homo sapiens		University of Iowa					
			451 Eckstein Medical Research Building Iowa City, IA 52242, USA					
			Tel: 319 335 8250					
			Fax: 319 335 9565					
			Email: msoares@blue.weeg.uiowa.edu					
REFERENCE	Dias Neto,E., Garcia, Correa,R., Verjovski-Almeida,S., Briones,M.R.,		Tissue Procurement: Dr. Gregg Hageman					
AUTHORS	Nagai,M.A., da Silva,W.Jr., Zigo,M.A., Bordin,S., Costa,F.F.,		CDNA Library preparation: Dr. M. Bento Soares, University of Iowa					
	Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,		CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa					
	Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare		DNA Sequencing by: Dr. M. Bento Soares, University of Iowa					
	'M.J., Soares,F., Brentani,R.R., Reis,I.F., de Souza,S.J. and		Clone Distribution: Researchers may obtain clones from Research					
	Simpson,A.J.		Genetics (www.resgen.com).					
TITLE			Seq Primer: M13 Reverse.					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		FEATURES	Location/Qualifiers				
MEDLINE	2020663		source	1..447				
COMMENT	Contact: Simpson A.J.G.		/organism="Homo Sapiens"					
	Ludwig Institute for Cancer Genetics		/db_xref="taxon:9606"					
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil		/clone="UI-E-CII-afq-d-05-0-UT"					
	Tel: +55-11-2704922		/clone_lib="UI-E-CII"					
	Fax: +55-11-2707001		/tissue_type="RPE and Choroid"					
	Email: asimpson@ludwig.org.br		/dev_stage="adult"					
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:		/lab_host="DH10B (Life Technologies) (T1 phage resistant."					
	(http://www.ludwig.org.br/scripts/getml2?P1?71=6&T=RC6-MT0061-310)		/note="Organ: eye; Vector: pMT73-Pac (Pharmacia) with a modified polylinker; Site_1: ECO R I; Site_2: Not I; UI-E-CII is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6,791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pMT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dA)18 tail. The sequence tag for this library is ACCPA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NET)."					
FEATURES			/db_xref="adult"					
source			/dev_stage="adult"					
	/organism="Homo sapiens"		/clone.lib="MR0061"					
	/db_xref="adult"		/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by Cloning products derived from ORBESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					

SOURCE	human.	Plate:LLAM10739 row: 0 column: 17
ORGANISM	Homo sapiens	High quality sequence stop: 655.
MATERIALS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Location/Qualifiers
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1. .657
AUTHORS	Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.	/organism="Homo sapiens"
TITLE	EST (Blum, et al.)	/db_xref="taxon:4825960"
JOURNAL	Unpublished (1999)	/clone_id="NIH_MGC_97"
COMMENT	Contact: Blum H	/lab_host="DH10B"
MIPS	Am Klopferspitze 18a D-82152 Martinsried, Germany	/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-I/HOI (gtcgag This is the 5' sequence of the clone insert
	Clone from S. Wiemann Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;	/db_xref="taxon:5'-TTTTTTTTTNTVN-3' , size-selected for average insert size 2.2 kb and normalized to Row 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
FEATURES		
source		
1. .653	Query Match Score 90; DB 12; Length 657;	
	Best Local Similarity 100.0%; Pred. No. 7.1e-13;	
	Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	QY 1 GGGAGACGGCGGGGTGGCCGGAGAGCAAGGAGCGGGATCCACTCGCAC A 60	
	Db 64 GGAGACGGCGGGTGGCCGGAGAGCAAGGAGCGGGATCCACTCGCAC A 123	
	QY 61 GCAGCGACTCGTGGCCGCCAGGTG 90	
	Db 124 GCAGCGACTCGTGGCCGCCAGGTG 153	
BASE COUNT	150 a 183 c 198 g 121 t 1 others	
ORIGIN		
		RESULT 8
		BI559391
		LOCUS 603253071.F1 NIH_MGC_97
		DEFINITION mRNA sequence.
		BI559391
		ACCESSION BI:15446705
		KEYWORDS EST.
		SOURCE human.
		ORGANISM Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 677)	
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D.	
	Email: cgabs-r@mail.nih.gov	
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	
	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:	
	http://image.llnl.gov	
	Plate: LLAM1747 row: n column: 18	
	High quality sequence stop: 677.	
FEATURES		
source		
1. .677	/organism="Homo sapiens"	
	/db_xref="taxon:9056"	
	/clone IMAGE:5295569"	
	/clone_id="NIH_MGC_97"	
	/lab_host="DH10B"	
REFERENCE	/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-I/HOI (gtcgag	
AUTHORS	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)	
TITLE	DNA Sequencing by: The I.M.A.G.E. Consortium (LILN)	
JOURNAL	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)	
COMMENT	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:	
	http://image.llnl.gov	

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, *In preparation*). Library was constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.^a

SULT 9 597041	BT597041 CDS DEFINITION mRNA sequence. B1597041 BT597041..1 EST.	679 bp mRNA Homo sapiens cDNA clone IMAGE:5300177 5', NIH_MGC_96 mRNA sequence. B1597041 BT597041..1 EST.	linear EST 07-SEP-2001 Homo sapiens GI:15489980	mRNA clone IMAGE:5300177 5', NIH_MGC_96 Homo sapiens GI:15489980	Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominoidea; Homo 1 (bases 1 to 679) NIH-MGC http://mgc.ncbi.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Organism Mammalia Eutheria Primates Catarrhini Hominoidea Homo Human.	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
						REFERENCE AUTHORS TITLE JOURNAL COMMENT	

Clone distribution: MGCl clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://Image.LINL.gov>
 Plate: L1AM1759 row: n column: 18
 High quality sequence stop: 675.
 Location/Qualifiers
 source - 1. .679

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5300177"
 /clone_lib="NIH_MGC_96"
 /tissue_type="hypothalamus"
 /lab_host="DRI0B"
 /note="Organ: brain; Vector: pBluecript-PIR (modified
 pBluecript KS+); Site:1: BamHI; Site:2: SalI-XbaI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.3 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIMH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 155 a 186 c 210 g 128 t

Query Match 100.0%; Score 90; DB 13; Length 679;
 Best Local Similarity 100.0%; Pred. No. 7.2e-13;
 Matches 90; Conservative 0; Mismatches 0; Indexes 0;
 Gaps 0;

VERSION BG719125.1 GI:13998312
KEYWORDS EST.
SOURCE human.
ORGANISM *Homo sapiens*

AUTHORS NIH-NCI <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: strausberg@nci.nih.gov

Tissue Procurement: Miklos Pavkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

Clone distribution: MGC clone distribution information can be obtained at www.ncbi.nlm.nih.gov/clone.
DNA Sequencing by: Incyte Genomics, Inc.

<http://image.llnl.gov>
Place: LLAM10753 row: c column: 15
High quality sequence stop: 684

FAILURES	SOURCE	LOCATION/QUARRIERS	1-685
1	1	1	1

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/clone_label: 403UV40  
/clone_l1b="NIH_MGC_97"  
/lab_host="DH10B"
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PBluescript KS+); Site_1: BamHI; Site_2: Sali-XHOI (gtccaa); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',

normalized to ROT 5. This is a Primary library enriched for full-length clones and constructed using the Cap-trapper method (Carrincli, in preparation). Library

BASE COUNT 160 a 184 c 204 g 137 t
Institutes of Health). Note: this is a NIH_MGC library."
constructed by Dr. J. W. Schatzkin (National Institutes of Health), National

Query Match Best Local Similarity 100.0% Score 90; DB 12; Length 685;

Db	6	GGGAGACGGGGGTGGGGCGGGGAGAGCAAGGACGGGGATCCACTCGCACA	65
Qy	61	GCAGGCCACTGGTGCCCGGCCAGGCTCG	90

RESULT 11
BM172428 LOCUS BM172428 mRNA linear EST - 04 - DEC - 200

found through the I.M.A.G.E. Consortium/LNLL at:

			/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgag pBluescript KS+); Row: m column: 20
			High quality sequence stop: 697.
FEATURES	Location/Qualifiers	1..715	
source	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_lib="NIH_MGC_96"		
	/tissue_type="hypothalamus"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgag pBluescript KS+); Row: m column: 20		
			i: Oligo-dT primed using primer 5'-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT	162 a	193 c	224 g
ORIGIN	162 t	137 t	137 t
			Query Match 100.0%; Score 90; DB 13; Length 716;
			Best Local Similarity 100.0%; Pred. No. 7.2e-13; Gaps 0;
			Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
			QY 1 GGGAGACGGGGGCGGGGGAGAGGAAGGAGCCACTCGGCCA 60
			DB 60 GGAGAGCGGGGGTGCGGCCGGAGAGCAAGGAGCCACTCGCCA 119
			QY 61 GCAGGCCACTCGTGCCCCGGAGGGTCC 90
			Db 120 GCAGGCCACTCGTGCCCCGGAGGGTCC 149
			RESULT 15
			Best Local Similarity 100.0%; Pred. No. 7.2e-13; Gaps 0;
			Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
			BG704185 LOCUS BG704185 mRNA 734 bp Homo sapiens IMAGE:4819374 5'-2001 DEFINITION 602687727F1 NIH_MGC_95 mRNA sequence.
			ACCESSION BG704185 VERSION BG704185.1 GI:13977267 COMMENT
			ORGANISM Homo sapiens
			Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
			REFERENCE 1 (bases 1 to 734) NIH-MGC http://mgc.ncbi.nih.gov/ AUTHORS TITLE JOURNAL Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgbps-1@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Yoshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLL at: http://image.llnl.gov/Plate: LIAM10724 row: f column: 07 High quality sequence stop: 701. Location/Qualifiers 1..734
			/organism="Homo sapiens"
			/db_xref="taxon:9606"
			/clone="IMAGE:4819374"
			/clone_lib="NIH_MGC_95"
			/tissue_type="hippocampus"
			/lab_host="DH10B"
			/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XbaI (gtcgag pBluescript KS+); Row: k column: 16
			High quality sequence stop: 99.
FEATURES	Location/Qualifiers	1..716	
source	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5284359"		
	/clone_lib="NIH_MGC_95"		
	/tissue_type="hippocampus"		
	/lab_host="DH10B"		
			BASE COUNT 165 a
			227 g
			ORIGIN 199 c

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Query Match      100.0%; Score 90; DB 12; Length 734;
Best Local Similarity 100.0%; Pred. No. 7.3e-13;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGAGAACGGCGCGGCGGGCGGGAGCAAGGACGGCCGCGGATCCACTCGCACA 60
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          64 GGGAGAACGGCGCGGCGGGAGCAAGGACGGCCGCGGATCCACTCGCACA 123
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy          61 GCAGGGCACCTCGGCGGCCCGGCAGGGTCG 90
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db          124 GCAGGGCACCTCGGCGGCCCGGCAGGGTCG 153
           ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: July 12, 2003, 21:58:09
Job time : 1450 secs